

**Metabolic Insights into *Desulfovibrio* from  
Genome Sequence**

**Judy D. Wall, Christopher Hemme, Barbara Rapp-  
Giles, and Rayford Payne**

Biochemistry Department  
University of Missouri-Columbia

**Supported by: U.S. Department of Energy  
NABIR Program**

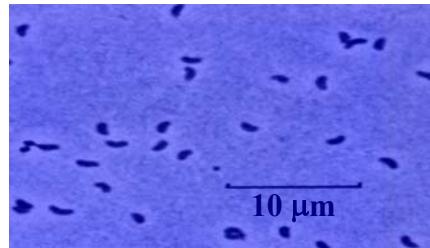


**Sequence data obtained from  
The Institute for Genomic Research**

**John L. Heidelberg**

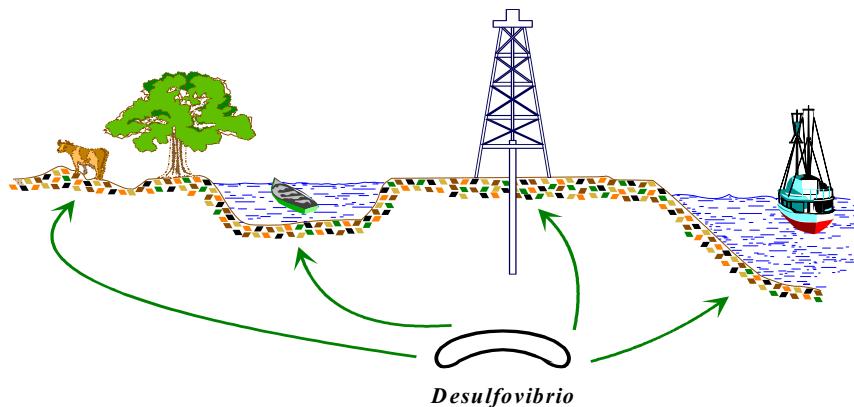
<http://www.tigr.org>

## *Desulfovibrio vulgaris*

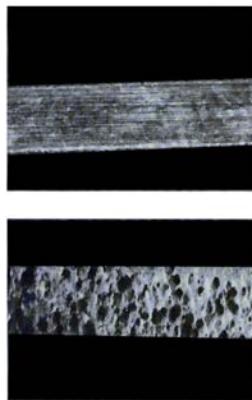


- 👉 Gram -
- 👉 Anaerobic
- 👉 Sulfate Reducing Bacteria (SRB)

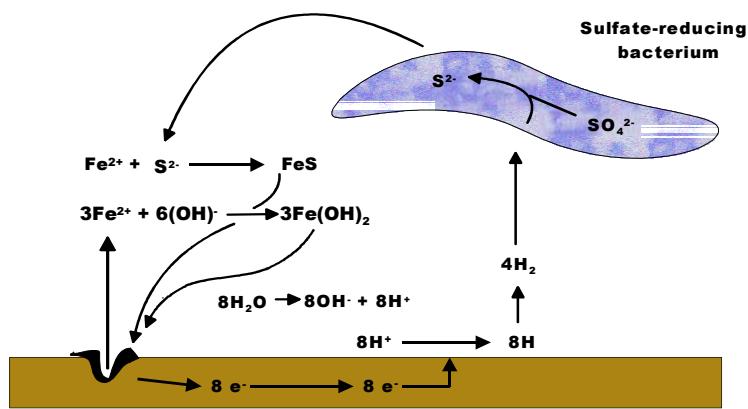
## Sulfate-Reducing Bacteria in Nature



Mild steel corrosion by  
*Desulfovibrio desulfuricans* G20



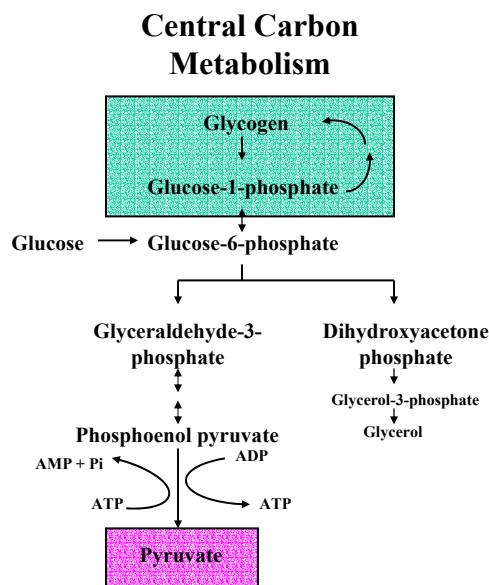
Cathodic Depolarization Model  
of Metal Corrosion



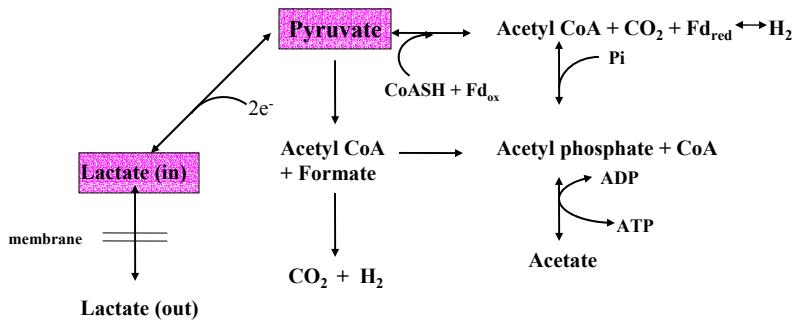
***Desulfovibrio vulgaris***  
**Hildenborough**

**Chromosome:** **3.57 Mb**  
**63.2% GC**  
**3527 ORFs**

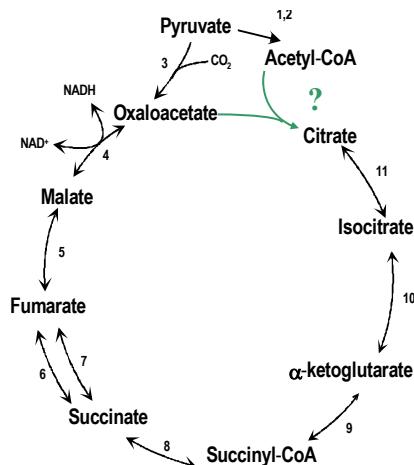
**Megaplasmid:** **203 Kb**  
**65.7% GC**  
**147 ORFs**



### Preferred Carbon Substrates of *Desulfovibrio*



### *Desulfovibrio vulgaris* Hildenborough TCA Cycle

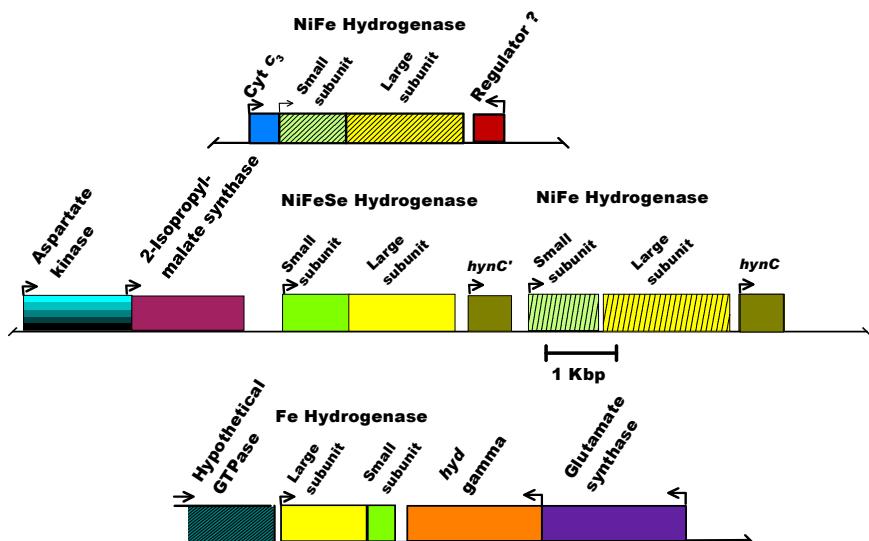


## Initial model of *Desulfovibrio* reduction of uranium

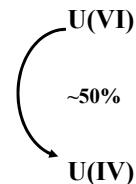
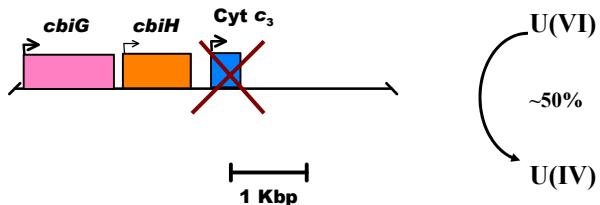


Lovley et al., 1993

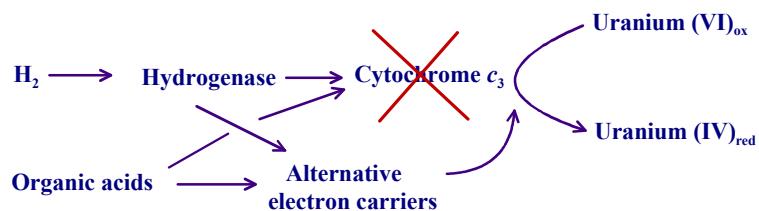
### *Desulfovibrio vulgaris* Hildenborough



*Desulfovibrio* Tetraheme  
Cytochrome *c*<sub>3</sub>



Modified model of *Desulfovibrio*  
reduction of uranium



*Desulfovibrio vulgaris*  
Hildenborough

Tetraheme c-type Cytochromes

ORF03638	.....LNRS.....TLMRY LVIS.....LFAVSL 19
ORF05080	.....LTRHGGHH TIPLGKSLTY LDEGGSSIMR K...LFFCGV 35
ORF03170	.....VRSHRTPLTE KTP <sup>Y</sup> LYHGRY IRHHGGSAMR S...AIRWGL 37
ORF04250	MAAWRTSSTI TNWG <sup>C</sup> TPSSS ATSSTTAWS PVRSSARPTK ENAMFRRGIT 50
ORF03638	LMAGSALGN AADAAKAPKK AIELKGTSK R.....MHV MFNHTTH... 60
ORF05080	LALAVAFALP VVAAPKAPAD GLKMEA..TR .....QPV VFHNSTH... 73
ORF03170	LTL . VLLSP ALAAAYDVPK EIEIKRPAKI KPVASWWGPV KFPNGFH... 82
ORF04250	VMLAFATLAL LLVAFAARTD TPRLEPEALKI PQQR...PAA VFDHDIAHNEK 97
ORF03638	KDIA. TEQCH HDSPAPDKP. ....YAST DND <sup>C</sup> HATPGP RERDTMSMFV 105
ORF05080	KSVK. CSDH HPVNKGKD. ....YRKCG TAG <sup>C</sup> DSMDK KDKSAKCYE 115
ORF03170	AIHNFKRACH HEEDSKLSIGS FLP. ....CS ..QCNKPGD AEQMSFYRAW 125
ORF04250	ARLEN <sup>C</sup> AVEH HDAKDGKIVP EGSSEGTPA ..D <sup>C</sup> HARAAT KGTHLVNAYE 145
ORF03638	AY <sup>C</sup> AKD.TDR S <sup>C</sup> YCC <sup>C</sup> HKM A...AQHPEF TGCRP. CHM SQQARKEAAA SEKK 15
ORF05080	VM <sup>C</sup> DKNTEFK S <sup>C</sup> VGC <sup>C</sup> NEVA GADAACKKDL TGCKKS <sup>C</sup> HE ..... 15
ORF03170	..H..NDKAY S <sup>C</sup> MGCCRQKR LLK. QGEPP IS <sup>C</sup> TR. G <sup>C</sup> HP LPTGGAQ 16
ORF04250	....RQ.. .C <sup>C</sup> MV <sup>C</sup> HTSG .....KGP TS <sup>C</sup> GG. CHV RD 16

ORF03638 – Downstream of FDH operon

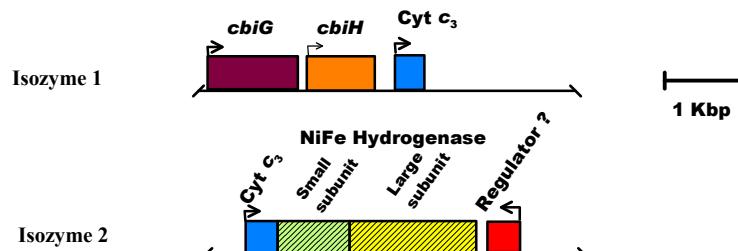
ORF05080 – Acidic isozyme

ORF03170 – Upstream of NiFe Hydrogenase genes

ORF04250 – Dominant cytochrome *c*<sub>3</sub>

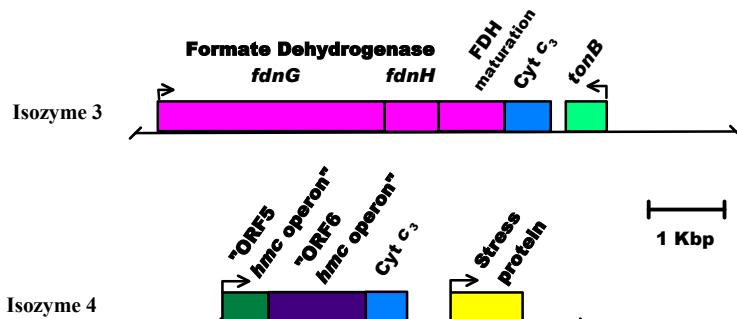
*Desulfovibrio vulgaris*  
Hildenborough

Tetraheme Cytochromes *c*



***Desulfovibrio vulgaris***  
**Hildenborough**

Tetraheme Cytochromes *c*



**Putative Terminal Reductases of  
*Desulfovibrio vulgaris* Hildenborough**

Sulfate Reductase  
Sulfite Reductase  
Thiosulfate Reductase  
Fumarate Reductase  
Dimethyl Sulfoxide Reductase  
Nitrite Reductase (?)  
Rubredoxin Oxygen Oxidoreductase  
Cytochrome *c* Oxidase  
Cytochrome *bd* Ubiquinol Oxidase

## **Pathogenic Features ???**

<b>Hemolysin</b>	2 ORFs (One upstream of an ABC transport system)
<b>Cytolysin</b>	RtxD-like (Associated with an ABC transport system)
<b>Type III secretion</b>	Eight ORFs located on the megaplasmid
<b>Hemagglutinin</b>	
<b>Adhesion lipoprotein</b>	